

10/17/2003

SEQUENCE LISTING

SEQ ID NO: 1 is mouse TECK nucleotide sequence.
SEQ ID NO: 2 is mouse TECK amino acid sequence.
SEQ ID NO: 3 is human TECK nucleotide sequence.
SEQ ID NO: 4 is human TECK amino acid sequence.
SEQ ID NO: 5 is human MIP-3 α nucleotide sequence.
SEQ ID NO: 6 is human MIP-3 α amino acid sequence.
SEQ ID NO: 7 is human MIP-3 β nucleotide sequence.
SEQ ID NO: 8 is human MIP-3 β amino acid sequence.
SEQ ID NO: 9 is human DC CR nucleotide sequence.
SEQ ID NO: 10 is human DC CR amino acid sequence.
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.
SEQ ID NO: 12 is human M/DC CR amino acid sequence.
SEQ ID NO: 13 is human CCKR1 amino acid sequence.
SEQ ID NO: 14 is human CCKR2 amino acid sequence.
SEQ ID NO: 15 is human CCKR3 amino acid sequence.
SEQ ID NO: 16 is human CCKR4 amino acid sequence.
SEQ ID NO: 17 is HPRT sense primer.
SEQ ID NO: 18 is HPRT antisense primer.
SEQ ID NO: 19 is FLAG epitope tag sequence.
SEQ ID NO: 20 is TECK sense primer
SEQ ID NO: 21 is TECK antisense primer
SEQ ID NO: 22 is exon 1-specific CRAM primer
SEQ ID NO: 23 is exon 2-specific CRAM primer
SEQ ID NO: 24 is exon 3-specific CRAM primer
SEQ ID NO: 25 is CRAM primer
SEQ ID NO: 26 is CRAM primer

<110> Wang, Wei

Gish, Kurt C.

Schall, Thomas J.

Vicari, Alain P.

Zlotnik, Albert

<120> Antibodies that bind chemokine TECK

<130> DX0589K1B US

<140> US 10/039,659

<141> 2002-01-03

<150> US 08/887,977

<151> 1997-07-03

<150> US 60/021,664

<151> 1996-07-05

<150> US 60/028,329

<151> 1996-10-11

<150> US 60/048,593

<151> 1997-06-04

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<170> PatentIn version 3.1

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Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
35 40 45

Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
50 55 60

Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
65 70 75 80

Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
85 90 95

Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
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Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
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 Met

 aac ctg tgg ctc ctg gcc tgc ctg gtg gcc ggc ttc ctg gga gcc tgg 167
 Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala Trp
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 gcc ccc gct gtc cac acc caa ggt gtc ttt gag gac tgc tgc ctg gcc 215
 Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu Ala
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 tac cac tac ccc att ggg tgg gct gtg ctc cgg cgc gcc tgg act tac 263
 Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr Tyr
 15 20 25

 cggtatc cag gag gtg agc ggg agc tgc aat ctg cct gct gcg ata ttc 311
 Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile Phe
 30 35 40

 tac ctc ccc aag aga cac agg aag gtg tgt ggg aac ccc aaa agc agg 359
 Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser Arg
 45 50 55

 gag gtg cag aga gcc atg aag ctc ctg gat gct cga aat aag gtt ttt 407
 Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val Phe
 60 65 70

 gca aag ctc cac cac aac atg cag acc ttc caa gca ggc cct cat gct 455

Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His Ala			
75	80	85	90
gta aag aag ttg agt tct gga aac tcc aag tta tca tca tcc aag ttt			503
Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe			
95	100	105	
agc aat ccc atc agc agc aag agg aat gtc tcc ctc ctg ata tca			551
Ser Asn Pro Ile Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser			
110	115	120	
gct aat tca gga ctg tgagccgct catttctggg ctccatccgc acaggagggg			606
Ala Asn Ser Gly Leu			
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ccggatcttt ctccgataaa accgtcgccc tacagaccca gctgtccca cgcctctgtc			666
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ctcactttct gtttcttgcc gtccaccccg ggccatgcca gtgtgtcctc tgggtcccct			906
ccaaaaatct ggtcattcaa ggatcccctc ccaaggctat gctttctat aactttaaa			966
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-5	-1	1	5

Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr			
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Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile			
30	35	40	

Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
45 50 55

Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
60 65 70

Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
75 80 85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
90 95 100 105

Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
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Ser Ala Asn Ser Gly Leu
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cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc 96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
-10 -5 -1 1 5

tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc 144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10 15 20

ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc 192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
25 30 35

ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act 240
Phe His Thr Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
40 45 50

tgg gtg aaa tat att gtg cgt ctc agt aaa aaa gtc aag aac atg 288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55 60 65 70

taaaaaactgt ggctttctg gaatggaatt ggacatagcc caagaacaga aagaaccttg 348
ctggggttgg aggtttcact tgcacatcat ggagggttta gtgcttatct aatttgc 408
tcactggact tgtccaatta atgaagttga ttcatattgc atcatagttt gctttgttta 468
agcatcacat taaagttaaa ctgtattta tgttatttat agctgttagt tttctgtgtt 528
tagctattta atactaattt tccataagct attttggttt agtgaaagt ataaaattat 588
atttgggggg gaataagatt atatggactt ttttgcagg aacaagctat tttttaaaaa 648
aaactattta acattttt gtttatattt ttttgcattcc taaattgttg taattgcatt 708
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 -10 -5 -1 1 5

Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20

Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35

Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
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gcctgcctct gttcaccctc c atg gcc ctg cta ctg gcc ctc agc ctg ctg 171
 Met Ala Leu Leu Leu Ala Leu Ser Leu Leu
 1 5 10

gtt ctc tgg act tcc cca gcc cca act ctg agt ggc acc aat gat gct 219
 Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala
 15 20 25

gaa gac tgc tgc ctg tct gtg acc cag aaa ccc atc cct ggg tac atc 267
 Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile
 30 35 40

gtg agg aac ttc cac tac ctt ctc atc aag gat ggc tgc agg gtg cct 315
 Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro
 45 50 55

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gct gta gtg ttc acc aca ctg agg ggc cgc cag ctc tgt gca ccc cca      363
Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro
   60           65           70

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gac cag ccc tgg gta gaa cgc atc atc cag aga ctg cag agg acc tca	411
Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser	
75 80 85 90	

gcc aag atg aag cgc cgc agc agt taacctatga ccgtgcagag ggagcccgga 465
Ala Lys Met Lys Arg Arg Ser Ser
95

gtccgagtca agcattgtga attattacct aacctgggaa accgaggacc agaaggaagg 525

accaggcttc cagctccctc gcaccagacc tgaccagcca ggacagggcc tggggtgtgt 585

gtgagtgta gtgtgagcga gagggtgagt gtggtctaga gtaaaagctgc tccacccca 645

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35 40 45

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
50 55 60

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
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att act cag ttg att ctg aga tgt tac tgt gct cct tgc agg agg tca 96
 Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
 20 25 30

ggc agt tct cca ggc tat ttg tac cga att gcc tac tcc ttg atc tgt 144
 Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
 35 40 45

gtt ctt ggc ctc ctg ggg aat att ctg gtg gtg atc acc ttt gct ttt 192
 Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
 50 55 60

tat aag aag gcc agg tct atg aca gac gtc tat ctc ttg aac atg gcc 240
 Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
 65 70 75 80

att gca gac atc ctc ttt gtt ctt act ctc cca ttc tgg gca gtg agt 288

Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser			
85	90	95	
cat gcc act ggt gcg tgg gtt ttc agc aat gcc acg tgc aag ttg cta			336
His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu			
100	105	110	
aaa ggc atc tat gcc atc aac ttt aac tgc ggg atg ctg ctc ctg act			384
Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr			
115	120	125	
tgc att agc atg gac cggt tac atc gcc att gta cag gcg act aag tca			432
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser			
130	135	140	
ttc cgg ctc cga tcc aga aca cta ccg cgc agc aaa atc atc tgc ctt			480
Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu			
145	150	155	160
gtt gtg tgg ggg ctg tca gtc atc atc tcc agc tca act ttt gtc ttc			528
Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe			
165	170	175	
aac caa aaa tac aac acc caa ggc agc gat gtc tgt gaa ccc aag tac			576
Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr			
180	185	190	
caa act gtc tcg gag ccc atc agg tgg aag ctg ctg atg ttg ggg ctt			624
Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu			
195	200	205	
gag cta ctc ttt ggt ttc ttt atc cct ttg atg ttg atg ata ttt tgt			672
Glu Leu Leu Phe Gly Phe Ile Pro Leu Met Phe Met Ile Phe Cys			
210	215	220	
tac acg ttc att gtc aaa acc ttg gtg caa gct cag aat tct aaa agg			720
Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg			
225	230	235	240
cac aaa gcc atc cgt gta atc ata gct gtg ctt gtg ttt ctg gct			768
His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala			
245	250	255	
tgt cag att cct cat aac atg gtc ctg ctt gtg acg gct gct aat ttg			816
Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu			
260	265	270	
ggt aaa atg aac cga tcc tgc cag agc gaa aag cta att ggc tat acg			864
Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr			
275	280	285	
aaa act gtc aca gaa gtc ctg gct ttc ctg cac tgc tgc ctg aac cct			912
Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro			
290	295	300	
gtg ctc tac gct ttt att ggg cag aag ttc aga aac tac ttt ctg aag			960

Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	
305					310				315					320		
atc	ttg	aag	gac	ctg	tgg	tgt	gtg	aga	agg	aag	tac	aag	tcc	tca	ggc	1008
Ile	Leu	Lys	Asp	Leu	Trp	Cys	Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly	
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ttc	tcc	tgt	gcc	ggg	agg	tac	tca	gaa	aac	att	tct	cg	cag	acc	agt	1056
Phe	Ser	Cys	Ala	Gly	Arg	Tyr	Ser	Glu	Asn	Ile	Ser	Arg	Gln	Thr	Ser	
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gag	acc	gca	gat	aac	gac	aat	gcg	tcg	tcc	ttc	act	atg	tgatagaaag		1105	
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Gly	Ser	Ser	Pro	Gly	Tyr	Leu	Tyr	Arg	Ile	Ala	Tyr	Ser	Leu	Ile	Cys	
					35			40				45				
Val	Leu	Gly	Leu	Leu	Gly	Asn	Ile	Leu	Val	Val	Ile	Thr	Phe	Ala	Phe	
						50			55			60				
Tyr	Lys	Lys	Ala	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	Ala	
						65			70			75		80		
Ile	Ala	Asp	Ile	Leu	Phe	Val	Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	Ser	
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His	Ala	Thr	Gly	Ala	Trp	Val	Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Leu	
						100			105				110			

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
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Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
 130 135 140

Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
 145 150 155 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
 165 170 175

Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
 180 185 190

Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
 195 200 205

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys
 210 215 220

Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
 225 230 235 240

His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala
 245 250 255

Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu
 260 265 270

Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr
 275 280 285

Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
 290 295 300

Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys
 305 310 315 320

Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
 325 330 335

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 Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala
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 cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat 153
 Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
 20 25 30 35
 gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag 201
 Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln
 40 45 50
 ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac 249
 Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp
 55 60 65
 aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc 297
 Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg
 70 75 80
 gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc 345

Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	
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Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	Ala	Gly	Gly	Asp	Pro	Met	Cys	
100				105					110					115		
aaa	att	ctc	att	gga	ctg	tac	tgc	gtg	ggc	ctg	tac	agt	gag	aca	ttt	441
Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	Gly	Leu	Tyr	Ser	Glu	Thr	Phe	
120				125				125			130					
ttc	aat	tgc	ctt	ctg	act	gtg	caa	agg	tac	cta	gtg	ttt	ttg	cac	aag	489
Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys	
135				140				140			145					
ggc	aac	ttt	ttc	tca	gcc	agg	agg	gtg	ccc	tgt	ggc	atc	att	aca		537
Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg	Val	Pro	Cys	Gly	Ile	Ile	Thr	
150				155				155			160					
agt	gtc	ctg	gca	tgg	gta	aca	gcc	att	ctg	gcc	act	ttg	cct	gaa	ttc	585
Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile	Leu	Ala	Thr	Leu	Pro	Glu	Phe	
165				170				170			175					
gtg	gtt	tat	aaa	cct	cag	atg	gaa	gac	cag	aaa	tac	aag	tgt	gca	ttt	633
Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp	Gln	Lys	Tyr	Lys	Cys	Ala	Phe	
180				185				185			190			195		
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Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp	Glu	Thr	Phe	Trp	Lys	His	Phe	
200				205				205			210					
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Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val	Leu	Val	Leu	Pro	Leu	Phe	Ile	
215				220				220			225					
ttt	aca	ttt	ctc	tat	gtg	caa	atg	aga	aaa	aca	cta	agg	ttc	agg	gag	777
Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg	Lys	Thr	Leu	Arg	Phe	Arg	Glu	
230				235				235			240					
cag	agg	tat	agc	ctt	tgc	aag	ctt	gtt	ttt	gcc	gta	atg	gta	gtc	ttc	825
Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Val	Met	Val	Val	Phe	
245				250				250			255					
ctt	ctg	atg	tgg	gcg	ccc	tac	aat	att	gca	ttt	ttc	ctg	tcc	act	ttc	873
Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe	
260				265				265			270			275		
aaa	gaa	cac	tcc	tcc	ctg	agt	gac	tgc	aag	agc	agc	tac	aat	ctg	gac	921
Lys	Glu	His	Phe	Ser	Leu	Ser	Asp	Cys	Lys	Ser	Ser	Tyr	Asn	Leu	Asp	
280				285				285			290					
aaa	agt	gtt	cac	atc	act	aaa	ctc	atc	gcc	acc	acc	cac	tgc	tgc	atc	969
Lys	Ser	Val	His	Ile	Thr	Lys	Leu	Ile	Ala	Thr	Thr	His	Cys	Cys	Ile	
295				300				300			305					
aac	cct	ctc	ctg	tat	gcg	ttt	ctt	gat	ggg	aca	ttt	agc	aaa	tac	ctc	1017

Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu			
310	315	320	
tgc cgc tgt ttc cat ctg cgt agt aac acc cca ctt caa ccc agg ggg			1065
Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly			
325	330	335	
cag tct gca caa ggc aca tcg agg gaa gaa cct gac cat tcc acc gaa			1113
Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu			
340	345	350	355
gtg taaaactagca tccaccaa at gcaagaagaa taaaacatgga ttttcatctt			1166
Val			
tctgcattat ttcatgtaaa ttttctacac atttgtatac aaaatcgat acaggaagaa			1226
aagggagagg tgagctaaca tttgctaagc actgaatttgc tctcaggcac cgtgcaaggc			1286
tctttacaaa cgtgagctcc ttgcctcctt accacttgc catagtgtgg ataggactag			1346
tctcatttctt ctgagaagaa aactaaggcg cgaaatttgc tctaagatca cataactagg			1406
aagtggcaga actgattctc cagccctggt agcatttgc tcttgcgttccat			1466
gaacatcaaaa ctccaaaccc tggggacaaa cgacatgaaa taaatgtatt taaaacata			1526
taaaaaaaaaaaa aaaaaaaaaaaa a			1547
<210> 12			
<211> 356			
<212> PRT			
<213> Homo sapiens			
<400> 12			
Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr			
1	5	10	15
Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu			
20	25	30	
Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu			
35	40	45	
Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly			
50	55	60	

Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
 65 70 75 80

Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
 85 90 95

Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
 100 105 110

Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
 115 120 125

Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
 130 135 140

Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
 145 150 155 160

Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
 165 170 175

Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
 180 185 190

Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
 195 200 205

Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
 210 215 220

Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
 225 230 235 240

Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met
 245 250 255

Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
 260 265 270

Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
 275 280 285

Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
 290 295 300

Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
 305 310 315 320

Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
 325 330 335

Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
 340 345 350

Ser Thr Glu Val
 355

<210> 13

<211> 355

<212> PRT

<213> Homo sapiens

<400> 13

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60

Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
 85 90 95

Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
 100 105 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Trp Ala Leu
 145 150 155 160

Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
 165 170 175

Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
 180 185 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
 195 200 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220

Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
 225 230 235 240

Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
 245 250 255

Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
 260 265 270

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
 275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
 305 310 315 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
 325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
 340 345 350

Ala Gly Phe
 355

<210> 14

<211> 374

<212> PRT

<213> Homo sapiens

<400> 14

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
 1 5 10 15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 20 25 30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 50 55 60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
 85 90 95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
355 360 365

Gln Asp Lys Glu Gly Ala
370

<210> 15

<211> 355

<212> PRT

<213> Homo sapiens

<400> 15

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
1 5 10 15

Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
20 25 30

Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
35 40 45

Leu Leu Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
 145 150 155 160

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
 165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
 180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
 195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
 225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
 245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
 260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
 275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
 305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
 325 330 335

Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
 340 345 350

Ile Val Phe
 355

<210> 16

<211> 360

<212> PRT

<213> Homo sapiens

<400> 16

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240

Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr
 245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350

Asp His Asp Leu His Asp Ala Leu
 355 360

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT sense primer

<400> 17

gtaatgatca gtcaacgggg gac

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT antisense primer

<400> 18

ccagcaagct tgcaacctta acca

24

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG epitope tag sequence

<400> 19

Asp Tyr Lys Asp Asp Asp Asp Lys Leu

1 5

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK sense primer

<400> 20

ccttcaggtt tctggagagg agatc

25

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK antisense primer

<400> 21

cacgcttgta ctgttgggggt tc

22

<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 1-specific CRAM primer

<400> 22

agacgcttca gagatcctct ggaggcc

27

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 2-specific CRAM primer

<400> 23
gaagctgctt cgggggggtga gcaaac 26

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 3-specific CRAM primer

<400> 24
caaacacagc agagcagagt gatggcacc 29

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 25
gtgtcctggc atgggttaaca gcc 23

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 26

cgggtggaaatg gtcagggttct tccc

24